



SEQUENCE LISTING

<110> Broglie, Richard Martin
DeBonte, Lorin Roger
Hitz, William Dean
Miao, Guo-Hua
Reiter, Robert Stefan

<120> Methods For Increasing Oleic Acid
Content In Seeds From Transgenic Plants Containing A Mutant
Delta 12 Desaturase

<130> 07148-025003

<140> US 09/643,579

<141> 2000-08-22

<150> US 09/232,948

<151> 1999-01-19

<150> US 08/728,025

<151> 1996-10-09

<160> 58

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1464

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (130)..(1281)

<400> 1

GGCACGAGCT CGTGCCGAAT TCGGCACGAG AGGAGACAGA GAGAGAGTTT GAGGAGGAGC 60

TTCTTCGTAG GGTTCATCGT TATTAACGTT AAATCTTCAT CCCCCCTAC GTCAGCCAGC 120

TCAAGAAAC ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC 168
Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser
1 5 10

AAA AAG TCT GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG 216
Lys Lys Ser Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro
15 20 25

CCC TTC ACT GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC 264
Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe
30 35 40 45

AAA CGC TCG ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC 312
Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile

50										55					60					
ATA	GCC	TCC	TGC	TTC	TAC	TAC	GTC	GCC	ACC	ACT	TAC	TTC	CCT	CTC	CTC	360				
Ile	Ala	Ser	Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu					
65				70				75												
CCT	CAC	CCT	CTC	TCC	TAC	TTC	GCC	TGG	CCT	CTC	TAC	TGG	GCC	TGC	CAG	408				
Pro	His	Pro	Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln					
80				85				90												
GGC	TGC	GTC	CTA	ACC	GGC	GTC	TGG	GTC	ATA	GCC	CAC	GAG	TGC	GGC	CAC	456				
Gly	Cys	Val	Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His					
95				100				105												
CAC	GCC	TTC	AGC	GAC	TAC	CAG	TGG	CTG	GAC	GAC	ACC	GTC	GGC	CTC	ATC	504				
His	Ala	Phe	Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile					
110				115				120				125								
TTC	CAC	TCC	TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAC	AGT	CAT	552				
Phe	His	Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His					
130				135				140												
CGA	CGC	CAC	CAT	TCC	AAC	ACT	GGC	TCC	CTC	GAG	AGA	GAC	GAA	GTG	TTT	600				
Arg	Arg	His	His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe					
145				150				155												
GTC	CCC	AAG	AAG	AAG	TCA	GAC	ATC	AAG	TGG	TAC	GGC	AAG	TAC	CTC	AAC	648				
Val	Pro	Lys	Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn					
160				165				170												
AAC	CCT	TTG	GGA	CGC	ACC	GTG	ATG	TTA	ACG	GTT	CAG	TTC	ACT	CTC	GGC	696				
Asn	Pro	Leu	Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly					
175				180				185												
TGG	CCT	TTG	TAC	TTA	GCC	TTC	AAC	GTC	TCG	GGG	AGA	CCT	TAC	GAC	GGC	744				
Trp	Pro	Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly					
190				195				200				205								
GGC	TTC	GCT	TGC	CAT	TTC	CAC	CCC	AAC	GCT	CCC	ATC	TAC	AAC	GAC	CGT	792				
Gly	Phe	Ala	Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg					
210				215				220												
GAG	CGT	CTC	CAG	ATA	TAC	ATC	TCC	GAC	GCT	GGC	ATC	CTC	GCC	GTC	TGC	840				
Glu	Arg	Leu	Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys					
225				230				235												
TAC	GGT	CTC	TAC	CGC	TAC	GCT	GCT	GTC	CAA	GGA	GTT	GCC	TCG	ATG	GTC	888				
Tyr	Gly	Leu	Tyr	Arg	Tyr	Ala	Ala	Val	Gln	Gly	Val	Ala	Ser	Met	Val					
240				245				250												
TGC	TTC	TAC	GGA	GTT	CCT	CTT	CTG	ATT	GTC	AAC	GGG	TTC	TTA	GTT	TTG	936				
Cys	Phe	Tyr	Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu					
255				260				265												
ATC	ACT	TAC	TTG	CAG	CAC	ACG	CAT	CCT	TCC	CTG	CCT	CAC	TAT	GAC	TCG	984				

Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser
 270 275 280 285

TCT GAG TGG GAT TGG TTG AGG GGA GCT TTG GCC ACC GTT GAC AGA GAC 1032
 Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp
 290 295 300

TAC GGA ATC TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG 1080
 Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val
 305 310 315

GCG CAT CAC CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT 1128
 Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala
 320 325 330

ACG AAG GCG ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG 1178
 Thr Lys Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly
 335 340 345

ACG CCG GTG GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT 1224
 Thr Pro Val Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr
 350 355 360 365

GTG GAA CCG GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC 1272
 Val Glu Pro Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn
 370 375 380

AAT AAG TTA TGAAGCAAAG AAGAACTGA ACCTTTCTCT TCTATGATTG 1321
 Asn Lys Leu

TCTTTGTTTA AGAAGCTATG TTTCTGTTTC AATAATCTTA ATTATCCATT TTGTTGTGTT 1381

TTCTGACATT TTGGCTAAAA TTATGTGATG TTGGAAGTTA GTGTCTAAAA AAAAAAAAAA 1441

AAAAAAAAAA AAAAAAAAAA AAA 1464

<210> 2
 <211> 384
 <212> PRT
 <213> Brassica napus

<400> 2
 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
 1 5 10 15

Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
 50 55 60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro

65	70	75	80
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	85	90	95
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	100	105	110
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	115	120	125
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	130	135	140
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	145	150	155
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	165	170	175
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	180	185	190
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	195	200	205
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	210	215	220
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	225	230	235
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr	245	250	255
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	260	265	270
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	275	280	285
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	290	295	300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	305	310	315
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	325	330	335
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	340	345	350
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	355	360	365
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu			

370

375

380

<210> 3

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(1152)

<400> 3

ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT	48
Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser	
1 5 10 15	
GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT	96
Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser	
50 55 60	
TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG GGC TGC GTC	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
CTA ACC GGC GTC TGG GTC ATA GCC CAC AAG TGC GGC CAC CAC GCC TTC	336
Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe	
100 105 110	
AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC TTC CAC TCC	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGA CGC CAC	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	

GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC GGC TTC GCT	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
TAC CGC TAC GCT GCT GTC CAA GGA GTT GCC TCG ATG GTC TGC TTC TAC	768
Tyr Arg Tyr Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
GGA GTT CCG CTT CTG ATT GTC AAT GGG TTC TTA GTT TTG ATC ACT TAC	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAC GAT TCG TCC GAG TGG	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
GAT TGG TTC AGG GGA GCT TTG GCC ACC GTT GAC AGA GAC TAC GGA ATC	912
Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG GCG CAT CAC	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
CTG TTC TCC ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT ACC AAG GCG	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	
ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
340 345 350	
GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	
GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T	1153
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu	
370 375 380	
GA	1155

<210> 4
<211> 384

<212> PRT

<213> Brassica napus

<400> 4

Met	Gly	Ala	Gly	Gly	Arg	Met	Gln	Val	Ser	Pro	Pro	Ser	Lys	Lys	Ser	
1				5					10					15		
Glu	Thr	Asp	Asn	Ile	Lys	Arg	Val	Pro	Cys	Glu	Thr	Pro	Pro	Phe	Thr	
			20					25					30			
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	
		35					40					45				
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser	
	50					55					60					
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro	
65					70					75					80	
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val	
				85					90					95		
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Lys	Cys	Gly	His	His	Ala	Phe	
			100					105					110			
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser	
	115					120						125				
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His	
	130					135					140					
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys	
145					150					155					160	
Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu	
				165					170					175		
Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu	
			180					185					190			
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Ala	
	195						200					205				
Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	
	210					215					220					
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu	
225					230					235					240	
Tyr	Arg	Tyr	Ala	Ala	Val	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr	
				245					250					255		
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr	
			260					265					270			
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	
		275					280					285				

Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

<210> 5
 <211> 1155
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(1152)

<400> 5
 ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT 48
 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
 1 5 10 15
 GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT 96
 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 20 25 30
 GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG 144
 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45
 ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC 192
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
 50 55 60
 TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT 240
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80
 CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAA GGG TGC GTC 288
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC CAC GCC TTC 336
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe

100				105				110									
AGC	GAC	TAC	CAG	TGG	CTT	GAC	GAC	ACC	GTC	GGT	CTC	ATC	TTC	CAC	TCC	384	
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser		
115				120				125									
TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAC	AGT	CAT	CGC	AGC	CAC	432	
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Ser	His		
130				135				140									
CAT	TCC	AAC	ACT	GGC	TCC	CTC	GAG	AGA	GAC	GAA	GTG	TTT	GTC	CCC	AAG	480	
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys		
145				150				155				160					
AAG	AAG	TCA	GAC	ATC	AAG	TGG	TAC	GGC	AAG	TAC	CTC	AAC	AAC	CCT	TTG	528	
Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu		
165				170				175									
GGA	CGC	ACC	GTG	ATG	TTA	ACG	GTT	CAG	TTC	ACT	CTC	GGC	TGG	CCG	TTG	576	
Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu		
180				185				190									
TAC	TTA	GCC	TTC	AAC	GTC	TCG	GGA	AGA	CCT	TAC	GAC	GGC	GGC	TTC	CGT	624	
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Arg		
195				200				205									
TGC	CAT	TTC	CAC	CCC	AAC	GCT	CCC	ATC	TAC	AAC	GAC	CGC	GAG	CGT	CTC	672	
Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu		
210				215				220									
CAG	ATA	TAC	ATC	TCC	GAC	GCT	GGC	ATC	CTC	GCC	GTC	TGC	TAC	GGT	CTC	720	
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu		
225				230				235				240					
TTC	CGT	TAC	GCC	GCC	GGC	CAG	GGA	GTG	GCC	TCG	ATG	GTC	TGC	TTC	TAC	768	
Phe	Arg	Tyr	Ala	Ala	Gly	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr		
245				250				255				260					
GGA	GTC	CCG	CTT	CTG	ATT	GTC	AAT	GGT	TTC	CTC	GTG	TTG	ATC	ACT	TAC	816	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr		
260				265				270									
TTG	CAG	CAC	ACG	CAT	CCT	TCC	CTG	CCT	CAC	TAC	GAT	TCG	TCC	GAG	TGG	864	
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp		
275				280				285									
GAT	TGG	TTC	AGG	GGA	GCT	TTG	GCT	ACC	GTT	GAC	AGA	GAC	TAC	GGA	ATC	912	
Asp	Trp	Phe	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile		
290				295				300									
TTG	AAC	AAG	GTC	TTC	CAC	AAT	ATT	ACC	GAC	ACG	CAC	GTC	GCG	CAT	CAT	960	
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His		
305				310				315				320					
CCG	TTC	TCC	ACG	ATG	CCG	CAT	TAT	CAC	GCG	ATG	GAA	GCT	ACC	AAG	GCG	1008	
Pro	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala		
325				330				335									

ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG 1056
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350

GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG 1104
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365

GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T 1153
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

GA 1155

<210> 6

<211> 384

<212> PRT

<213> Brassica napus

<400> 6

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
 1 5 10 15

Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
 50 55 60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 165 170 175

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 275 280 285
 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

<210> 7
 <211> 1155
 <212> DNA
 <213> Brassica npaus

<220>
 <221> CDS
 <222> (1)..(1152)

<400> 7
 ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT 48
 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
 1 5 10 15
 GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT 96
 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 20 25 30
 GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG 144
 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser

35					40					45						
ATC	CCT	CGC	TCT	TTC	TCC	TAC	CTC	ATC	TGG	GAC	ATC	ATC	ATA	GCC	TCC	192
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser	
50					55					60						
TGC	TTC	TAC	TAC	GTC	GCC	ACC	ACT	TAC	TTC	CCT	CTC	CTC	CCT	CAC	CCT	240
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro	
65					70					75					80	
CTC	TCC	TAC	TTC	GCC	TGG	CCT	CTC	TAC	TGG	GCC	TGC	CAA	GGG	TGC	GTC	288
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val	
85					90					95						
CTA	ACC	GGC	GTC	TGG	GTC	ATA	GCC	CAC	GAG	TGC	GGC	CAC	CAC	GCC	TTC	336
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe	
100					105					110						
AGC	GAC	TAC	CAG	TGG	CTT	GAC	GAC	ACC	GTC	GGT	CTC	ATC	TTC	CAC	TCC	384
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser	
115					120					125						
TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAC	AGT	CAT	CGC	AGC	CAC	432
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Ser	His	
130					135					140						
CAT	TCC	AAC	ACT	GGC	TCC	CTC	GAG	AGA	GAC	GAA	GTG	TTT	GTC	CCC	AAG	480
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys	
145					150					155					160	
AAG	AAG	TCA	GAC	ATC	AAG	TGG	TAC	GGC	AAG	TAC	CAC	AAC	AAC	CCT	TTG	528
Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	His	Asn	Asn	Pro	Leu	
165					170					175						
GGA	CGC	ACC	GTG	ATG	TTA	ACG	GTT	CAG	TTC	ACT	CTC	GGC	TGG	CCG	TTG	576
Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu	
180					185					190						
TAC	TTA	GCC	TTC	AAC	GTC	TCG	GGA	AGA	CCT	TAC	GAC	GGC	GGC	TTC	CGT	624
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Arg	
195					200					205						
TGC	CAT	TTC	CAC	CCC	AAC	GCT	CCC	ATC	TAC	AAC	GAC	CGC	GAG	CGT	CTC	672
Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	
210					215					220						
CAG	ATA	TAC	ATC	TCC	GAC	GCT	GGC	ATC	CTC	GCC	GTC	TGC	TAC	GGT	CTC	720
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu	
225					230					235					240	
TTC	CGT	TAC	GCC	GCC	GGC	CAG	GGA	GTG	GCC	TCG	ATG	GTC	TGC	TTC	TAC	768
Phe	Arg	Tyr	Ala	Ala	Gly	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr	
245					250					255						
GGA	GTC	CCG	CTT	CTG	ATT	GTC	AAT	GGT	TTC	CTC	GTG	TTG	ATC	ACT	TAC	816
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr	
260					265					270						

TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAC GAT TCG TCC GAG TGG	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
GAT TGG TTC AGG GGA GCT TTG GCT ACC GTT GAC AGA GAC TAC GGA ATC	912
Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCC CAT CAT	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG	1008
Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	
ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
340 345 350	
GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	
GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T	1153
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu	
370 375 380	
GA	1155
<210> 8	
<211> 384	
<212> PRT	
<213> Brassica napus	
<400> 8	
Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser	
1 5 10 15	
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu
 165 170 175
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 275 280 285
 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

<210> 9
 <211> 23
 <212> DNA
 <213> Brassica napus

<400> 9 catgggtgca ggtggaagaa tgc	23
<210> 10 <211> 21 <212> DNA <213> Brassica napus	
<400> 10 gtttcttctt tgcttcataa c	21
<210> 11 <211> 23 <212> DNA <213> Brassica napus	
<400> 11 catgggtgca ggtggaagaa tgc	23
<210> 12 <211> 21 <212> DNA <213> Brassica napus	
<400> 12 tctttcacca tcatcatatc c	21
<210> 13 <211> 19 <212> DNA <213> Brassica napus	
<400> 13 gtctgggtca tagcccacg	19
<210> 14 <211> 19 <212> DNA <213> Brassica napus	
<400> 14 gtctgggtca tagcccaca	19
<210> 15 <211> 17 <212> DNA <213> Brassica napus	
<400> 15 ctgggtcata gcccatg	17

<210> 16
<211> 17
<212> DNA
<213> Brassica napus

<400> 16
ctgggtcata gcccaca

17

<210> 17
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> fragment

<221> Variant
<222> 2
<223> Xaa = Asp or Glu

<221> Variant
<222> 4
<223> Xaa = Ala or Gly

<400> 17
His Xaa Cys Xaa His
1 5

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 18
Ala Ile Pro Pro His Cys
1 5

<210> 19
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 19
Ala Ile Pro Lys His Cys
1 5

<210> 20
<211> 6
<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<221> VARIANT

<222> 4

<223> Xaa = Pro or Lys

<400> 20

Ala Ile Pro Xaa His Cys
1 5

<210> 21

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<221> VARIANT

<222> 3

<223> Xaa = Leu or Ile

<400> 21

Trp Pro Xaa Tyr Trp
1 5

<210> 22

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<400> 22

Trp Pro Leu Tyr Trp
1 5

<210> 23

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<400> 23

Ala His Glu Cys Gly His
1 5

<210> 24

<211> 6

<212> PRT

<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 24
Gly His Asp Cys Gly His
1 5

<210> 25
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> 1
<223> Xaa = Ala or Gly

<221> VARIANT
<222> 3
<223> Xaa = Asp or Glu

<400> 25
Xaa His Xaa Cys Gly His
1 5

<210> 26
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 26
Leu Leu Val Pro Tyr
1 5

<210> 27
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 27
Ile Leu Val Pro Tyr
1 5

<210> 28
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> 1
<223> Xaa = Leu or Ile

<400> 28
Xaa Leu Val Pro Tyr
1 5

<210> 29
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 29
Trp Lys Tyr Ser His Arg
1 5

<210> 30
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 30
Trp Arg Ile Ser His Arg
1 5

<210> 31
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> 2
<223> Xaa = Lys or Arg

<221> VARIANT
<222> 3
<223> Xaa = Tyr or Ile

<400> 31
Trp Xaa Xaa Ser His Arg
1 5

<210> 32
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 32
Ser His Arg Arg His His
1 5

<210> 33
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 33
Ser His Arg Thr His His
1 5

<210> 34
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> 4
<223> Xaa = Arg or Thr

<400> 34
Ser His Arg Xaa His His
1 5

<210> 35
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 35
Ile Thr Tyr Leu Gln
1 5

<210> 36
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 36
 Val Thr Tyr Leu His
 1 5

<210> 37
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence

<221> VARIANT
 <222> 1
 <223> Xaa = Ile or Val

<221> VARIANT
 <222> 5
 <223> Xaa = Gln or His

<400> 37
 Xaa Thr Tyr Leu Xaa
 1 5

<210> 38
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence

<400> 38
 Leu Pro His Tyr
 1

<210> 39
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence

<400> 39
 Leu Pro Trp Tyr
 1

<210> 40
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence

<221> VARIANT
 <222> 3
 <223> Xaa = His or Trp

 <400> 40
 Leu Pro Xaa Tyr
 1

 <210> 41
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Consensus sequence

 <221> VARIANT
 <222> 3
 <223> Xaa = Arg or Lys

 <400> 41
 Trp Leu Xaa Gly Ala Leu
 1 5

 <210> 42
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Consensus sequence

 <400> 42
 Tyr Leu Arg Gly Gly Leu
 1 5

 <210> 43
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Consensus sequence

 <221> VARIANT
 <222> 1
 <223> Xaa = Trp or Tyr

 <221> VARIANT
 <222> 3
 <223> Xaa = Arg or Lys

 <221> VARIANT
 <222> 5
 <223> Xaa = Ala or Gly

 <400> 43

Xaa Leu Xaa Gly Xaa Leu
1 5

<210> 44
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 44
Thr Val Asp Arg Asp Tyr Gly
1 5

<210> 45
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 45
Thr Leu Asp Arg Asp Tyr Gly
1 5

<210> 46
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> 2
<223> Xaa = Val or Leu

<400> 46
Thr Xaa Asp Arg Asp Tyr Gly
1 5

<210> 47
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 47
Thr His Val Ala His His Leu Phe
1 5

<210> 48
<211> 8

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Consensus sequence

 <400> 48
 Thr His Val Ile His His Leu Phe
 1 5

 <210> 49
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Consensus sequence

 <221> VARIANT
 <222> 4
 <223> Xaa = Ala or Ile

 <400> 49
 Thr His Val Xaa His His Leu Phe
 1 5

 <210> 50
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Consensus sequence

 <400> 50
 His His Leu Phe Ser Thr Met Pro His Tyr
 1 5 10

 <210> 51
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Consensus sequence

 <400> 51
 His His Leu Phe Pro Gln Ile Pro His Tyr
 1 5 10

 <210> 52
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Consensus sequence

<221> VARIANT
 <222> 5
 <223> Xaa = Ser or Pro

 <221> VARIANT
 <222> 6
 <223> Xaa = Thr or Gln

 <221> VARIANT
 <222> 7
 <223> Xaa = Ile or Met

 <400> 52
 His His Leu Phe Xaa Xaa Xaa Pro His Tyr
 1 5 10

 <210> 53
 <211> 5
 <212> PRT
 <213> Brassica napus

 <220>

 <400> 53
 His Glu Cys Gly His
 1 5

 <210> 54
 <211> 5
 <212> PRT
 <213> Brassica napus

 <220>

 <400> 54
 His Asp Cys Ala His
 1 5

 <210> 55
 <211> 5
 <212> PRT
 <213> Brassica napus

 <400> 55
 His Asp Cys Gly His
 1 5

 <210> 56
 <211> 12
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 56

tggtcttttg gt

12

<210> 57

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 57

gtcgacgagg

10

<210> 58

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 58

agatctggta cc

12